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OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 12:54:54 ; Search time 108 Seconds
(without alignments)
5594.172 Million cell updates/sec

Title: US-09-931-232-2
Perfect score: 850
Sequence: 1 atggtgagcaaggaggagga.....taggatcaatgttagatgc 850

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	850	100.0	850	3	US-09-062-102-2
2	850	100.0	850	3	US-09-364-946-2
3	718.6	84.5	761	4	US-09-869-588-25
4	718.6	84.5	5069	4	US-09-393-483A-1
5	718.6	84.5	5069	4	US-09-393-483A-2
6	718.6	84.5	7015	4	US-09-770-315-1
7	718.6	84.5	9423	4	US-09-377-066-6
8	718	84.5	4397	4	US-09-503-799-1
9	717.4	84.4	720	3	US-09-172-063-11
10	717.4	84.4	720	4	US-09-316-919-12
11	717.4	84.4	720	4	US-09-602-641-11
12	717.4	84.4	720	4	US-09-920-922-1
13	717.4	84.4	720	4	US-09-316-920A-12
14	717.4	84.4	972	3	US-09-172-063-29
15	717.4	84.4	972	4	US-09-602-641-29
16	717.4	84.4	1095	3	US-09-085-305-5
17	717.4	84.4	1140	4	US-09-417-197-128
18	717.4	84.4	1635	4	US-09-417-197-112
19	717.4	84.4	1815	4	US-09-417-197-58
20	717.4	84.4	1821	4	US-09-417-197-64
21	717.4	84.4	1893	4	US-09-417-197-62
22	717.4	84.4	1929	2	US-08-818-253-1
23	717.4	84.4	1929	2	US-08-818-253-5
24	717.4	84.4	1929	3	US-08-818-252-1
25	717.4	84.4	1929	3	US-08-818-252-5
26	717.4	84.4	2043	4	US-09-800-170-47
27	717.4	84.4	2157	4	US-09-417-197-74

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28 717.4 84.4 2181 4 US-09-417-197-70 Sequence 70, Appl
29 717.4 84.4 2394 4 US-09-417-197-140 Sequence 140, App
30 717.4 84.4 2397 4 US-09-417-197-76 Sequence 76, Appl
31 717.4 84.4 2511 4 US-09-417-197-60 Sequence 60, Appl
32 717.4 84.4 2562 4 US-09-417-197-118 Sequence 118, App
33 717.4 84.4 2592 3 US-09-591-025-8 Sequence 8, Appl
34 717.4 84.4 2592 4 US-09-894-927B-8 Sequence 8, Appl
35 717.4 84.4 2598 4 US-09-417-197-136 Sequence 136, App
36 717.4 84.4 2799 4 US-09-417-197-110 Sequence 110, App
37 717.4 84.4 2913 4 US-09-417-197-66 Sequence 66, Appl
38 717.4 84.4 2991 4 US-09-417-197-122 Sequence 122, App
39 717.4 84.4 3138 4 US-09-417-197-78 Sequence 78, Appl
40 717.4 84.4 3546 4 US-09-417-197-132 Sequence 132, App
41 717.4 84.4 4748 4 US-09-796-575-4 Sequence 4, Appl
42 717.4 84.4 4992 4 US-09-796-575-5 Sequence 5, Appl
43 717.4 84.4 8614 3 US-09-208-827-5 Sequence 5, Appl
44 717.4 84.4 8614 4 US-10-043-074-5 Sequence 5, Appl
45 717.4 84.4 9687 3 US-09-133-944-2 Sequence 2, Appl

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ALIGNMENTS

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RESULT 1
; US-09-062-102-2
; Sequence 2, Application US/09062102
; Patent No. 6130313
; GENERAL INFORMATION:
; APPLICANT: Kain, Steve
; APPLICANT: Li, Xianqiang
; TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: D6100
; CURRENT APPLICATION NUMBER: US/09/062,102
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: US 60/060,855
; EARLIER FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 2
; LENGTH: 850
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence which encodes the EGFP-MODC422-461
; OTHER INFORMATION: fusion protein.
; US-09-062-102-2

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Query Match 100.0%; Score 850; DB 3; Length 850;
Best Local Similarity 100.0%; Pred. No. 1.6e-168;
Matches 850; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGAGCAAGGCGAGGAGCTGTTCCACGGGGTGTGCCCATCTCTGTCGAGCTGCAC 60
Db 1 ATGTGAGCAAGGCGAGGAGCTGTTCCACGGGGTGTGCCCATCTCTGTCGAGCTGCAC 60
Qy 61 GGGACGTAACCGGCCCAAGTTTCAGCGTGTCCGGGAGGCGGAGGCGGATGCCACCTAC 120
Db 61 GGGACGTAACCGGCCCAAGTTTCAGCGTGTCCGGGAGGCGGAGGCGGATGCCACCTAC 120
Qy 121 GGCAGCTGACCTGAGTTTCATCTGCACCGGAGGAGTGCCTGCGCTGCCGCCACC 180
Db 121 GGCAGCTGACCTGAGTTTCATCTGCACCGGAGGAGTGCCTGCGCTGCCGCCACC 180
Qy 181 CTGCTGACCACTGACCTACGCGCTGCACTGTTTCAGCGCTACCCCGACCATGAAG 240
Db 181 CTGCTGACCACTGACCTACGCGCTGCACTGTTTCAGCGCTACCCCGACCATGAAG 240
Qy 241 CAGCAGCTTCTTAAAGTCCGCCATGCCGAAGGTTACGTCCAGGAGGCCACCATCTTC 300
Db 241 CAGCAGCTTCTTAAAGTCCGCCATGCCGAAGGTTACGTCCAGGAGGCCACCATCTTC 300
Qy 301 TTCAAGGACGAGGCACTACAGACCGCGCGAGGTGAAGTTCGAGGCGACACCTG 360

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Db	301	TTCAAGGACGACGGCAACTACAAGACCGCGCCGAGGTGAATTCGAGGGCGACACCCCTG	360	Db	61	GGCAGCTAAACGGCCACAAAGTTCAAGCTGTCCGCGAGGGCGAGGGCGATGCCACTAC	120
QY	361	GTGAACCCATCGAGCTGAAGGGATCGACTTCAAGGAGGACGGCAACATCTCTGGGGCAC	420	QY	121	GGCAAGCTGACCCCTGAAGTTTATCTGCACCAACCGCAAGCTGCCCTGCCCTGGCCACC	180
Db	361	GTGAACCCATCGAGCTGAAGGGATCGACTTCAAGGAGGACGGCAACATCTCTGGGGCAC	420	Db	121	GGCAAGCTGACCCCTGAAGTTTATCTGCACCAACCGCAAGCTGCCCTGCCCTGGCCACC	180
QY	421	AAGCTGGAGTACAACTACAACAGCCACAAACGTTTATATCATGGCCGACAAAGCAGAAGAAC	480	QY	181	CTCGTGACCAACCTGACCTAGCGGTGAGTGTTCAGCGGTACCCCGACACACATGAAG	240
Db	421	AAGCTGGAGTACAACTACAACAGCCACAAACGTTTATATCATGGCCGACAAAGCAGAAGAAC	480	Db	181	CTCGTGACCAACCTGACCTAGCGGTGAGTGTTCAGCGGTACCCCGACACACATGAAG	240
QY	481	GGCATCAAGGTCAACTTCAAGATCCGCCACACATCGAGGACGGCGTGCAGCTCGCC	540	QY	241	CAGCACGACTTCTTCAAGTCCGCCATGCCGAAGCTAGCTCCAGGAGCGCAACATCTTC	300
Db	481	GGCATCAAGGTCAACTTCAAGATCCGCCACACATCGAGGACGGCGTGCAGCTCGCC	540	Db	241	CAGCACGACTTCTTCAAGTCCGCCATGCCGAAGCTAGCTCCAGGAGCGCAACATCTTC	300
QY	541	GACCACTACACAGCAACACCCCATCGCGACGGCCCGTGTCTGTGCCCCACACACAC	600	QY	301	TTCAAGGACGACGGCAACTACAAGACCGCGCCGAGGTGAATTCGAGGGCGACACCCCTG	360
Db	541	GACCACTACACAGCAACACCCCATCGCGACGGCCCGTGTCTGTGCCCCACACACAC	600	Db	301	TTCAAGGACGACGGCAACTACAAGACCGCGCCGAGGTGAATTCGAGGGCGACACCCCTG	360
QY	601	TACCTGAGCACCCAGTCCCGCTGAGCAAGACCCCAACGAGGACGGCGATGATGGCACGCTGCCCATGTCT	660	QY	361	GTGAACCCATCGAGCTGAAGGGATCGACTTCAAGGAGGACGGCAACATCTCTGGGGCAC	420
Db	601	TACCTGAGCACCCAGTCCCGCTGAGCAAGACCCCAACGAGGACGGCGATGATGGCACGCTGCCCATGTCT	660	Db	361	GTGAACCCATCGAGCTGAAGGGATCGACTTCAAGGAGGACGGCAACATCTCTGGGGCAC	420
QY	661	CTGCTGGAGTTCGTGACCCCGCGGGATCACTCTCGGCATGACGAGCTGTACAGAAG	720	QY	421	AAGCTGGAGTACAACTACAACAGCCACAAACGTTTATATCATGGCCGACAAAGCAGAAGAAC	480
Db	661	CTGCTGGAGTTCGTGACCCCGCGGGATCACTCTCGGCATGACGAGCTGTACAGAAG	720	Db	421	AAGCTGGAGTACAACTACAACAGCCACAAACGTTTATATCATGGCCGACAAAGCAGAAGAAC	480
QY	721	CTTAGCCATGGCTTCCCGCGGAGGTGAGGACGAGGATGATGGCACGCTGCCCATGTCT	780	QY	481	GGCATCAAGGTCAACTTCAAGATCCGCCACACATCGAGGACGGCGTGCAGCTCGCC	540
Db	721	CTTAGCCATGGCTTCCCGCGGAGGTGAGGACGAGGATGATGGCACGCTGCCCATGTCT	780	Db	481	GGCATCAAGGTCAACTTCAAGATCCGCCACACATCGAGGACGGCGTGCAGCTCGCC	540
QY	781	TGTGCCAGGAGCGGGATGACCGTACCCCTGACGCTGTCTCTCTAGGATCAAT	840	QY	541	GACCACTACACAGCAACACCCCATCGCGACGGCCCGTGTCTGTGCCCCACACACAC	600
Db	781	TGTGCCAGGAGCGGGATGACCGTACCCCTGACGCTGTCTCTCTAGGATCAAT	840	Db	541	GACCACTACACAGCAACACCCCATCGCGACGGCCCGTGTCTGTGCCCCACACACAC	600
QY	841	GTGTAGATGC 850		QY	601	TACCTGAGCACCCAGTCCCGCTGAGCAAGACCCCAACGAGGACGGCGATGATGGCACGCTGCCCATGTCT	660
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RESULT 3							
US-09-869-588-25							
; Sequence 25, Application US/09869588							
; Patent No. 6790657							
; GENERAL INFORMATION:							
; APPLICANT: Ariya							
; TITLE OF INVENTION: Lentivirus Vector System							
; FILE REFERENCE: 59316							
; CURRENT APPLICATION NUMBER: US/09/869,588							
; CURRENT FILING DATE: 2001-06-28							
; PRIOR APPLICATION NUMBER: PCT/US00/00390							
; PRIOR FILING DATE: 2000-01-06							
; PRIOR APPLICATION NUMBER: 60/115,247							
; PRIOR FILING DATE: 1999-01-07							
; NUMBER OF SEQ ID NOS: 32							
; SOFTWARE: Patentin Ver. 2.1							
; SEQ ID NO 25							
; LENGTH: 761							
Query Match 100.0%; Score 850; DB 3; Length 850;							
Best Local Similarity 100.0%; Pred. No. 1.6e-168;							
Matches 850; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
QY	1	ATGGTGAAGGCGGAGGAGCTTTACCGGGTGTGTGCCATCTCTGTCGAGCTGGAC	60	QY	841	GTGTAGATGC 850	
Db	1	ATGGTGAAGGCGGAGGAGCTTTACCGGGTGTGTGCCATCTCTGTCGAGCTGGAC	60	Db	841	GTGTAGATGC 850	
QY	61	GGGACCTAACGGCCCAAGTTCAGCTGTCCCGGAGGCGAGGCGGATGCCACCTAC	120	QY	61	GGCAGCTAAACGGCCACAAAGTTCAAGCTGTCCGCGAGGGCGAGGGCGATGCCACTAC	120

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: mutant green
; OTHER INFORMATION: fluorescent protein
US-09-869-588-25

Query Match      84.5%; Score 718.6; DB 4; Length 761;
Best Local Similarity 98.8%; Pred. No. 3.7e-141;
Matches 724; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTGTAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTCCCATCTCTGTCGAGCTGGAC 60
Db 20 ATGTGTAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTCCCATCTCTGTCGAGCTGGAC 79
QY 61 GGCAGCTGTAACCGGCCCAAGTTTCAGCGGTGTCCGGCGAGGCGGCGATGCCACCTAC 120
Db 80 GGCAGCTGTAACCGGCCCAAGTTTCAGCGGTGTCCGGCGAGGCGGCGATGCCACCTAC 139
QY 121 GGCAGCTGTAACCGGCCCAAGTTTCAGCGGTGTCCGGCGAGGCGGCGATGCCACCTAC 180
Db 140 GGCAGCTGTAACCGGCCCAAGTTTCAGCGGTGTCCGGCGAGGCGGCGATGCCACCTAC 199
QY 181 CTGCTGACCACTGACCTACCGGTGTGAGTGTTCAGCGGTGTCCGGCGAGGCGGCGATGCCACCTAC 240
Db 200 CTGCTGACCACTGACCTACCGGTGTGAGTGTTCAGCGGTGTCCGGCGAGGCGGCGATGCCACCTAC 259
QY 241 CAGCAGCACTTCTTCAAGTCCGCGCATGCCCGAAGGCTACGTCAGGAGCGGCGATGCCACCTAC 300
Db 260 CAGCAGCACTTCTTCAAGTCCGCGCATGCCCGAAGGCTACGTCAGGAGCGGCGATGCCACCTAC 319
QY 301 TTCAAGGACGACGCGCACTCAAGACCGCGCGCGAGTGAAGTTTCGAGGCGGCGATGCCACCTAC 360
Db 320 TTCAAGGACGACGCGCACTCAAGACCGCGCGCGAGTGAAGTTTCGAGGCGGCGATGCCACCTAC 379
QY 361 GTCAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGAGCGCAACATCTCTGGGGCAC 420
Db 380 GTCAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGAGCGCAACATCTCTGGGGCAC 439
QY 421 AAGCTGAGTACAACTCAACAGCCCAACAGCTCTATATCATGGCCGCAAGCAGAAGAAC 480
Db 440 AAGCTGAGTACAACTCAACAGCCCAACAGCTCTATATCATGGCCGCAAGCAGAAGAAC 499
QY 481 GGCATCAAGGTGAATCTCAAGATCCGCCCAACATCGAGGAGCGGCGATGCCACCTAC 540
Db 500 GGCATCAAGGTGAATCTCAAGATCCGCCCAACATCGAGGAGCGGCGATGCCACCTAC 559
QY 541 GACCACTTACCAAGCAAGAACACCCCATCGCGAGCGGCCCGGTGTGTGCTGCCGCAACCCAC 600
Db 560 GACCACTTACCAAGCAAGAACACCCCATCGCGAGCGGCCCGGTGTGTGCTGCCGCAACCCAC 619
QY 601 TACCTGAGCAACCGAGTCCGCCCTGAGCAAGACCCCAAGAGAGCGCGATCACATGGTC 660
Db 620 TACCTGAGCAACCGAGTCCGCCCTGAGCAAGACCCCAAGAGAGCGCGATCACATGGTC 679
QY 661 CTGCTGAGTTCGTGACCGCGCGCGGATCACTCTCGGATGACGAGCTGTACAAGAG 720
Db 680 CTGCTGAGTTCGTGACCGCGCGCGGATCACTCTCGGATGACGAGCTGTACAAGAG 739
QY 721 CTTAGCCATGGCT 733
Db 740 AGCGGCGCGGACT 752
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RESULT 4

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US-09-393-483A-1
; Sequence 1, Application US/09393483A
; Patent No. 6689936
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Amano, Satoshi
; APPLICANT: Kishimoto, Jiro
; APPLICANT: Nishiyama, Toshio
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; APPLICANT: Ehama, Ritsuko
; TITLE OF INVENTION: METHODS FOR EVALUATING A COMPOUND FOR
; FILE OF INVENTION: ITS EFFECT ON SKIN
; FILE REFERENCE: 10287-054001
; CURRENT APPLICATION NUMBER: US/09/393,483A
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 09/070,436
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/069,945
; PRIOR FILING DATE: 1997-12-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5069
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-393-483A-1

Query Match      84.5%; Score 718.6; DB 4; Length 5069;
Best Local Similarity 98.8%; Pred. No. 5.4e-141;
Matches 724; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTGTAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTCCCATCTCTGTCGAGCTGGAC 60
Db 1015 ATGTGTAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTCCCATCTCTGTCGAGCTGGAC 1074
QY 61 GGCAGCTGTAACCGGCCCAAGTTTCAGCGGTGTCCGGCGAGGCGGCGATGCCACCTAC 120
Db 1075 GGCAGCTGTAACCGGCCCAAGTTTCAGCGGTGTCCGGCGAGGCGGCGATGCCACCTAC 1134
QY 121 GGCAGCTGTAACCGGCCCAAGTTTCAGCGGTGTCCGGCGAGGCGGCGATGCCACCTAC 180
Db 1135 GGCAGCTGTAACCGGCCCAAGTTTCAGCGGTGTCCGGCGAGGCGGCGATGCCACCTAC 1194
QY 181 CTGCTGACCACTGACCTACCGGTGTGAGTGTTCAGCGGTGTCCGGCGAGGCGGCGATGCCACCTAC 240
Db 1195 CTGCTGACCACTGACCTACCGGTGTGAGTGTTCAGCGGTGTCCGGCGAGGCGGCGATGCCACCTAC 1254
QY 241 CAGCAGCACTTCTTCAAGTCCGCGCATGCCCGAAGGCTACGTCAGGAGCGGCGATGCCACCTAC 300
Db 1255 CAGCAGCACTTCTTCAAGTCCGCGCATGCCCGAAGGCTACGTCAGGAGCGGCGATGCCACCTAC 1314
QY 301 TTCAAGGACGACGCGCACTCAAGACCGCGCGCGAGTGAAGTTTCGAGGCGGCGATGCCACCTAC 360
Db 1315 TTCAAGGACGACGCGCACTCAAGACCGCGCGCGAGTGAAGTTTCGAGGCGGCGATGCCACCTAC 1374
QY 361 GTCAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGAGCGCAACATCTCTGGGGCAC 420
Db 1375 GTCAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGAGCGCAACATCTCTGGGGCAC 1434
QY 421 AAGCTGAGTACAACTCAACAGCCCAACAGCTCTATATCATGGCCGCAAGCAGAAGAAC 480
Db 1435 AAGCTGAGTACAACTCAACAGCCCAACAGCTCTATATCATGGCCGCAAGCAGAAGAAC 1494
QY 481 GGCATCAAGGTGAATCTCAAGATCCGCCCAACATCGAGGAGCGGCGATCACATGGTC 540
Db 1495 GGCATCAAGGTGAATCTCAAGATCCGCCCAACATCGAGGAGCGGCGATCACATGGTC 1554
QY 541 GACCACTTACCAAGCAAGAACACCCCATCGCGAGCGGCCCGGTGTGTGCTGCCGCAACCCAC 600
Db 1555 GACCACTTACCAAGCAAGAACACCCCATCGCGAGCGGCCCGGTGTGTGCTGCCGCAACCCAC 1614
QY 601 TACCTGAGCAACCGAGTCCGCCCTGAGCAAGACCCCAAGAGAGCGCGATCACATGGTC 660
Db 1615 TACCTGAGCAACCGAGTCCGCCCTGAGCAAGACCCCAAGAGAGCGCGATCACATGGTC 1674
QY 661 CTGCTGAGTTCGTGACCGCGCGCGGATCACTCTCGGATGACGAGCTGTACAAGAG 720
Db 1675 CTGCTGAGTTCGTGACCGCGCGCGGATCACTCTCGGATGACGAGCTGTACAAGAG 1734
QY 721 CTTAGCCATGGCT 733
Db 1735 AGCGGCGCGGACT 1747
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Db 3651 GGCATCAAGTGAATTCAGATCGGCCAACAATCGAGGACGGCAGCGTGCAGTCCGC 3710
Qy 541 GACCACTACAGCAGAGAACACCCCATCGGCGACGCGCCCGTGTCTGCTGCCCGACAACCCAC 600
Db 3711 GACCACTACAGCAGAGAACACCCCATCGGCGACGCGCCCGTGTCTGCTGCCCGACAACCCAC 3770
Qy 601 TACCTGAGCACCAGTCCGCTCGAGCAAGAACACCCACGAGAGCGCGATCAGTGTGC 660
Db 3771 TACCTGAGCACCAGTCCGCTCGAGCAAGAACACCCACGAGAGCGCGATCAGTGTGC 3830
Qy 661 CTGCTGGAGTTCGTGACCGCGCCCGGATCACTCTCGGCATGGACGAGCTGTACAAGAAG 720
Db 3831 CTGCTGGAGTTCGTGACCGCGCCCGGATCACTCTCGGCATGGAGAGCTGTACAAGTAA 3890
Qy 721 CTTAGCCATGGCT 733
Db 3891 AGCGCGCGGACT 3903

RESULT 7
US-09-377-066-6
; Sequence 6, Application US/09377066A
; Patent No. 6773914
; GENERAL INFORMATION:
; APPLICANT: Handler, Alfred M.
; TITLE OF INVENTION: PiggyBac Transformation System
; FILE REFERENCE: 0194.98
; CURRENT APPLICATION NUMBER: US/09/377,066A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 6
; LENGTH: 9423
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence: pB(Pub-nls-BGFP)#257
US-09-377-066-6

Query Match 84.5%; Score 718.6; DB 4; Length 9423;
Best Local Similarity 98.8%; Pred. No. 6e-141;
Matches 724; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGGTGAGCAAGGGCGAGGAGCTGTTCAACCGGGTGTGTCCTCCTGCTGAGCTGGAC 60
Db 5377 ATGGTGAGCAAGGGCGAGGAGCTGTTCAACCGGGTGTGTCCTCCTGCTGAGCTGGAC 5436
Qy 61 GCGGACGTAAACGGCCACCAAGTTTCAGCGTGTCCGCGAGGGCGAGGCGGATGCCACCTAC 120
Db 5437 GCGGACGTAAACGGCCACCAAGTTTCAGCGTGTCCGCGAGGGCGAGGCGGATGCCACCTAC 5496
Qy 121 GGCAAGCTGACCTGAGTTCATCTGCACCAACCGGCAAGCTGCCCGTCCCTGCGCCCAACC 180
Db 5497 GGCAAGCTGACCTGAGTTCATCTGCACCAACCGGCAAGCTGCCCGTCCCTGCGCCCAACC 5556
Qy 181 CTGCTGACCAACCTGACCTACGGGTGCACTGTTTACCGCTGTCACCCGACCAATGAAG 240
Db 5557 CTGCTGACCAACCTGACCTACGGGTGCACTGTTTACCGCTGTCACCCGACCAATGAAG 5616
Qy 241 CAGCAGACTTCTTCAAGTCCCGCATGCCGAGGCTACGTCAGGAGCGCACCATCTTC 300
Db 5617 CAGCAGACTTCTTCAAGTCCCGCATGCCGAGGCTACGTCAGGAGCGCACCATCTTC 5676
Qy 301 TTCAAGGACGACGGCACTACAAGACCGCGCGGAGTGAAGTTTCGAGGCGCACACCCCTG 360
Db 5677 TTCAAGGACGACGGCACTACAAGACCGCGCGGAGTGAAGTTTCGAGGCGCACACCCCTG 5736
Qy 361 GTGAAACCGCATCAGCTGAAGGGGATCGACTTCAAGGAGGACGGCAACATCTTGGGGCAC 420
Db 5737 GTGAAACCGCATCAGCTGAAGGGGATCGACTTCAAGGAGGACGGCAACATCTTGGGGCAC 5796
Qy 421 AAGCTGAGGTACACTACACAGCCCAACGTCCTATATCATATGCGCCGACAGCAGAGAAC 480
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Db 5797 AAGCTGAGTAACTAACAAGCCCAACACGCTCTATATCATGGCCGACAAGCAGAGAAC 5856
Qy 481 GGCAATCAAGGTGAATCTCAAGATCCGCCACAACATCGAGGACGGCAGCTGCAGCTGCC 540
Db 5857 GGCAATCAAGGTGAATCTCAAGATCCGCCACAACATCGAGGACGGCAGCTGCAGCTGCC 5916
Qy 541 GACCACTACAGCAGAGAACACCCCATCGGCGACGCGCCCGTGTCTGCTGCCCGACAACCCAC 600
Db 5917 GACCACTACAGCAGAGAACACCCCATCGGCGACGCGCCCGTGTCTGCTGCCCGACAACCCAC 5976
Qy 601 TACCTGAGCACCAGTCCGCTCGAGCAAGAACACCCACGAGAGCGCGATCAGTGTGC 660
Db 5977 TACCTGAGCACCAGTCCGCTCGAGCAAGAACACCCACGAGAGCGCGATCAGTGTGC 6036
Qy 661 CTGCTGGAGTTCGTGACCGCGCCCGGATCACTCTCGGCATGGACGAGCTGTACAAGAAG 720
Db 6037 CTGCTGGAGTTCGTGACCGCGCCCGGATCACTCTCGGCATGGAGAGCTGTACAAGTAA 6096
Qy 721 CTTAGCCATGGCT 733
Db 6097 AGCGCGCGGACT 6109

RESULT 8
US-09-503-799-1
; Sequence 1, Application US/09503799
; Patent No. 6451563
; GENERAL INFORMATION:
; APPLICANT: Wittig, Burghardt
; APPLICANT: Junghans, Claas
; APPLICANT: Schroff, Matthias
; TITLE OF INVENTION: METHOD FOR MAKING LINEAR, COVALENTLY CLOSED DNA CONSTRUCTS
; FILE REFERENCE: NHL-NP-21
; CURRENT APPLICATION NUMBER: US/09/503,799
; CURRENT FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4397
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pUC 19 derivative, comprising a coding sequence for the modified
; OTHER INFORMATION: enhanced green fluorescence protein from aquaeoxa victoria under
; OTHER INFORMATION: control of cmv-promoter
US-09-503-799-1

Query Match 84.5%; Score 718; DB 4; Length 4397;
Best Local Similarity 100.0%; Pred. No. 7e-141;
Matches 718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGAGCAAGGGCGAGGAGCTGTTCAACCGGGTGTGTCCTCCTGCTGAGCTGGAC 60
Db 3073 ATGGTGAGCAAGGGCGAGGAGCTGTTCAACCGGGTGTGTCCTCCTGCTGAGCTGGAC 3132
Qy 61 GCGGACGTAAACGGCCACCAAGTTTCAGCGTGTCCGCGAGGGCGAGGCGGATGCCACCTAC 120
Db 3133 GCGGACGTAAACGGCCACCAAGTTTCAGCGTGTCCGCGAGGGCGAGGCGGATGCCACCTAC 3192
Qy 121 GGCAAGCTGACCTGAGTTCATCTGCACCAACCGGCAAGCTGCCCGTCCCTGCGCCCAACC 180
Db 3193 GGCAAGCTGACCTGAGTTCATCTGCACCAACCGGCAAGCTGCCCGTCCCTGCGCCCAACC 3252
Qy 181 CTGCTGACCAACCTGACCTACGGGTGCACTGTTTCAAGTCCCGCATGCCGCGTACCCCGACCATGAAG 240
Db 3253 CTGCTGACCAACCTGACCTACGGGTGCACTGTTTCAAGTCCCGCATGCCGCGTACCCCGACCATGAAG 3312
Qy 241 CAGCAGACTTCTTCAAGTCCCGCATGCCGCGTACGTCAGGAGGACGGCAACATCTTTC 300
Db 3313 CAGCAGACTTCTTCAAGTCCCGCATGCCGCGTACGTCAGGAGGACGGCAACATCTTTC 3372
Qy 301 TTCAAGGACGACGGCAACTACAAGACCGCGCGGAGTGAAGTTTCGAGGCGCACACCCCTG 360
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Db	3373	TTCAGGACGACGGCAACTACAAGACCCGCGGAGGTGAAGTTTCGAGGGCGACACCCCTG	3432	CTCGTGACCCCTGACCTACGGCTGAGTGTCTTACGCGCTACCCCGACACATGAAG	240
Qy	361	GTGAACCCATCGAGCTGAAGGGCATCGACTTCAAGAGGAGCGGCAACATCTCTGGGGCAC	420	CTCGTGACCAACCTGACCTACGGCTGAGTGTCTTACGCGCTACCCCGACACATGAAG	240
Db	3433	GTGAACCCATCGAGCTGAAGGGCATCGACTTCAAGAGGAGCGGCAACATCTCTGGGGCAC	3492	CAGCACGACTTCTTCAAGTCCGCCATGCCCAGAAAGCTACGTCAGAGGCGCACCATCTTC	300
Qy	421	AAGCTGGAGTAACTAACAAGCCACAACCGTCTATATCATGCGCGACAAGCAGAAGAAC	480	CAGCACGACTTCTTCAAGTCCGCCATGCCCAGAAAGCTACGTCAGAGGCGCACCATCTTC	300
Db	3493	AAGCTGGAGTAACTAACAAGCCACAACCGTCTATATCATGCGCGACAAGCAGAAGAAC	3552	TTCAGGACGAGCGCAACTACAAGACCCGCGCGAGGTGAAGTTTCGAGGGCGACACCCCTG	360
Qy	481	GGCATCAAGGTGAACCTCAAGATCCGCCACACATCGAGGAGCGGAGCGTGCAGCTCGCC	540	TTCAGGACGAGCGCAACTACAAGACCCGCGCGAGGTGAAGTTTCGAGGGCGACACCCCTG	360
Db	3553	GGCATCAAGGTGAACCTCAAGATCCGCCACACATCGAGGAGCGGAGCGTGCAGCTCGCC	3612	TTCAGGACGAGCGCAACTACAAGACCCGCGCGAGGTGAAGTTTCGAGGGCGACACCCCTG	360
Qy	541	GACCACTACCAAGCAGAAACACCCCATCGCGACGCGCCCGTCTGCTGCGCCGACACCCAC	600	GTGAACCCATCGAGCTGAAGGGCATCGACTTCAAGAGGAGCGGCAACATCTCTGGGGCAC	420
Db	3613	GACCACTACCAAGCAGAAACACCCCATCGCGACGCGCCCGTCTGCTGCGCCGACACCCAC	3672	GTGAACCCATCGAGCTGAAGGGCATCGACTTCAAGAGGAGCGGCAACATCTCTGGGGCAC	420
Qy	601	TACCTGAGACCCAGTCCGCCCTGAGCAAAAGACCCCAAGAGAGGGCGATCACATGGTC	660	AAGCTGGAGTAACTAACAAGCCACAACCGTCTATATCATGCGCGACAAGCAGAAGAAC	480
Db	3673	TACCTGAGACCCAGTCCGCCCTGAGCAAAAGACCCCAAGAGAGGGCGATCACATGGTC	3732	AAGCTGGAGTAACTAACAAGCCACAACCGTCTATATCATGCGCGACAAGCAGAAGAAC	480
Qy	661	CTGCTGGAGTTCGTGACCGCGCGCGGATCACTCTCGGCATGAGAGCTGTACAAGA	718	GGCATCAAGGTGAACCTCAAGATCCGCCACACATCGAGGAGCGGAGCGTGCAGCTCGCC	540
Db	3733	CTGCTGGAGTTCGTGACCGCGCGCGGATCACTCTCGGCATGAGAGCTGTACAAGA	3790	GGCATCAAGGTGAACCTCAAGATCCGCCACACATCGAGGAGCGGAGCGTGCAGCTCGCC	540
RESULT 9					
US-09-172-063-11					
; Sequence 11, Application US/09172063					
; Patent No. 6150176					
; GENERAL INFORMATION:					
; APPLICANT: Tsien, Roger Y.					
; APPLICANT: Miyawaki, Atsushi					
; APPLICANT: Llopis, Juan					
; APPLICANT: Wachter, Rebekka M.					
; APPLICANT: Remington, S. James					
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR					
; TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE					
; FILE REFERENCE: 07257/071001					
; CURRENT APPLICATION NUMBER: US/09/172,063					
; CURRENT FILING DATE: 1998-10-13					
; EARLIER APPLICATION NUMBER: 09/094,359					
; EARLIER FILING DATE: 1998-06-09					
; NUMBER OF SEQ ID NOS: 38					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 11					
; LENGTH: 720					
; TYPE: DNA					
; ORGANISM: Aequorea victoria					
; FEATURE:					
; NAME/KEY: misc feature					
; LOCATION: (0)..(0)					
; OTHER INFORMATION: EGFP					
US-09-172-063-11					
Query Match 84.4%; Score 717.4; DB 3; Length 720;					
Best Local Similarity 99.9%; Pred. No. 6.6e-141;					
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
Qy	1	ATGGTGAGCAAGGGCGAGGAGTGTTCACCGGGGTGGTCCCATCTCTGGTCGAGCTGGAC	60	1	ATGGTGAGCAAGGGCGAGGAGTGTTCACCGGGGTGGTCCCATCTCTGGTCGAGCTGGAC
Db	1	ATGGTGAGCAAGGGCGAGGAGTGTTCACCGGGGTGGTCCCATCTCTGGTCGAGCTGGAC	60	1	ATGGTGAGCAAGGGCGAGGAGTGTTCACCGGGGTGGTCCCATCTCTGGTCGAGCTGGAC
Qy	61	GGCGAGTAAAGCGGCGACAAAGTTCACTGCTCCGGGAGGGCGAGGCGATGCCACTAC	120	61	GGCGAGTAAAGCGGCGACAAAGTTCACTGCTCCGGGAGGGCGAGGCGATGCCACTAC
Db	61	GGCGAGTAAAGCGGCGACAAAGTTCACTGCTCCGGGAGGGCGAGGCGATGCCACTAC	120	61	GGCGAGTAAAGCGGCGACAAAGTTCACTGCTCCGGGAGGGCGAGGCGATGCCACTAC
Qy	121	GGCAAGCTGACCTGAAGTTCACTGCAACCGGCAAGCTGCCCGTCCCTGGCCCAACC	180	121	GGCAAGCTGACCTGAAGTTCACTGCAACCGGCAAGCTGCCCGTCCCTGGCCCAACC
Db	121	GGCAAGCTGACCTGAAGTTCACTGCAACCGGCAAGCTGCCCGTCCCTGGCCCAACC	180	121	GGCAAGCTGACCTGAAGTTCACTGCAACCGGCAAGCTGCCCGTCCCTGGCCCAACC
Qy	181	CTCGTGACCAACCTGACCTACGGCGTGCAGTGTTCAGCCGCTACCCCGACCATGAAG	240	181	CTCGTGACCAACCTGACCTACGGCGTGCAGTGTTCAGCCGCTACCCCGACCATGAAG

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Db 181 CTCGTGACCACTGACCTACCGCGTGCAGTCTTACGCCGTACCCCGACCAATGAAG 240
QY 241 CAGCAGCACTTCTTCAAGTCGCCATGCCCGGAAGGCTAGCTCCAGGAGCGCACTCTTC 300
Db 241 CAGCAGCACTTCTTCAAGTCGCCATGCCCGGAAGGCTAGCTCCAGGAGCGCACTCTTC 300
QY 301 TTCAGGAGCGGCGCAACTAGAGACCCCGCGGAGGTGAAGTTGAGGGCGACACCCCTG 360
Db 301 TTCAGGAGCGGCGCAACTAGAGACCCCGCGGAGGTGAAGTTGAGGGCGACACCCCTG 360
QY 361 GTGAACCGCATCGAGCTGAAGGCGCATCTCAAGGAGGAGCGCAACATCTCTGGGCGAC 420
Db 361 GTGAACCGCATCGAGCTGAAGGCGCATCTCAAGGAGGAGCGCAACATCTCTGGGCGAC 420
QY 421 AAGCTGGAGTCAACTCAACAGCCACCAACGCTCTATATCATGCGCCGCAAGCAGAGAAC 480
Db 421 AAGCTGGAGTCAACTCAACAGCCACCAACGCTCTATATCATGCGCCGCAAGCAGAGAAC 480
QY 481 GGCATCAAGGTGAACCTCAAGATCCGCCACACATCGAGGAGCGGAGCTGCGCTGCC 540
Db 481 GGCATCAAGGTGAACCTCAAGATCCGCCACACATCGAGGAGCGGAGCTGCGCTGCC 540
QY 541 GACCACTACCAAGCAACACCCCGCATCGCGGAGCGGCCCGCTGCTGCTGCCCGCAACAC 600
Db 541 GACCACTACCAAGCAACACCCCGCATCGCGGAGCGGCCCGCTGCTGCTGCCCGCAACAC 600
QY 601 TACCTGAGCAGCGAGTCCGCGCTGAGCAAGAACCCCAACGAGAGCGCGATGCTGC 660
Db 601 TACCTGAGCAGCGAGTCCGCGCTGAGCAAGAACCCCAACGAGAGCGCGATGCTGC 660
QY 661 CTGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGGCATGGAGCTGTACAAGAA 719
Db 661 CTGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGGCATGGAGCTGTACAAGAA 719
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RESULT 11

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US-09-602-641-11
; Sequence 11, Application US/09602641
; Patent No. 6608189
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; APPLICANT: Llopis, Juan
; APPLICANT: Wachter, Rebekka M.
; APPLICANT: Remington, S. James
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; MEASURING THE PH OF A BIOLOGICAL SAMPLE
; FILE REFERENCE: 07257/071001
; CURRENT APPLICATION NUMBER: US/09/602,641
; PRIOR FILING DATE: 2000-06-22
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: EGFP
US-09-602-641-11
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Query Match 84.4%; Score 717.4; DB 4; Length 720;
Best Local Similarity 99.9%; Pred. No. 6.6e-141;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGAGCAAGGCGGAGGAGCTGTTTCAACCGGGTGGTGGCCATCTCTGGTGGAGCTGGAC 60
Db 1 ATGTGAGCAAGGCGGAGGAGCTGTTTCAACCGGGTGGTGGCCATCTCTGGTGGAGCTGGAC 60
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QY 61 GCGCAGTAACCGGCCACAAGTTCAAGCGTGTCCGCGAGGGCGAGCGGCGATGCCACTAC 120
Db 61 GCGCAGTAACCGGCCACAAGTTCAAGCGTGTCCGCGAGGGCGAGGGCGATGCCACTAC 120
QY 121 GSCAAGCTGACCTCAAGTTTCATCTGCACACCGGCAAGTCCCGTGCCTGGCCCGCCAC 180
Db 121 GSCAAGCTGACCTCAAGTTTCATCTGCACACCGGCAAGTCCCGTGCCTGGCCCGCCAC 180
QY 181 CTCGTGACCACTGACCTACCGCGTGCAGTCTTTCAGCCGCTACCCCGACCAATGAAG 240
Db 181 CTCGTGACCACTGACCTACCGCGTGCAGTCTTTCAGCCGCTACCCCGACCAATGAAG 240
QY 241 CAGCAGCACTTCTTCAAGTCGCCATGCCCGGAAGGCTAGCTCCAGGAGCGCACTCTTC 300
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QY 301 TTCAGGAGCGGCGCAACTAGAGACCCCGCGGAGGTGAAGTTGAGGGCGACACCCCTG 360
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QY 361 GTGAACCGCATCGAGCTGAAGGCGCATCTCAAGGAGGAGCGCAACATCTCTGGGCGAC 420
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QY 421 AAGCTGGAGTCAACTCAACAGCCACCAACGCTCTATATCATGCGCCGCAAGCAGAGAAC 480
Db 421 AAGCTGGAGTCAACTCAACAGCCACCAACGCTCTATATCATGCGCCGCAAGCAGAGAAC 480
QY 481 GGCATCAAGGTGAACCTCAAGATCCGCCACACATCGAGGAGCGGAGCTGCGCTGCC 540
Db 481 GGCATCAAGGTGAACCTCAAGATCCGCCACACATCGAGGAGCGGAGCTGCGCTGCC 540
QY 541 GACCACTACCAAGCAACACCCCGCATCGCGGAGCGGCCCGCTGCTGCTGCCCGCAACAC 600
Db 541 GACCACTACCAAGCAACACCCCGCATCGCGGAGCGGCCCGCTGCTGCTGCCCGCAACAC 600
QY 601 TACCTGAGCAGCGAGTCCGCGCTGAGCAAGAACCCCAACGAGAGCGCGATGCTGC 660
Db 601 TACCTGAGCAGCGAGTCCGCGCTGAGCAAGAACCCCAACGAGAGCGCGATGCTGC 660
QY 661 CTGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGGCATGGAGCTGTACAAGAA 719
Db 661 CTGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGGCATGGAGCTGTACAAGAA 719
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RESULT 12

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US-09-920-922-1
; Sequence 1, Application US/09920922
; Patent No. 6673610
; GENERAL INFORMATION:
; APPLICANT: Miyawaki, Atsushi
; APPLICANT: Sawano, Asako
; TITLE OF INVENTION: METHOD FOR MUTAGENESIS
; FILE REFERENCE: 11283-012001
; CURRENT APPLICATION NUMBER: US/09/920,922
; CURRENT FILING DATE: 2001-08-02
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(717)
US-09-920-922-1
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Query Match 84.4%; Score 717.4; DB 4; Length 720;
Best Local Similarity 99.9%; Pred. No. 6.6e-141;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY	1	ATGTTGAGCAAGGGCGAGAGCTGTTTCAACCGGGTGGTGCCCATCTGTGTGAGCTGGAC	60
Db	1	ATGGTGAGCAAGGGCGAGAGCTGTTTCAACCGGGTGGTGCCCATCTGTGTGAGCTGGAC	60
QY	61	GGGACGTAAGAGGCCACAAAGTTGACGGTGTCCGGCGAGGGCGAGGGCGATGCCACCTAC	120
Db	61	GGGACGTAAGAGGGCGCAAAAGTTGACGGTGTCCGGCGAGGGCGAGGGCGATGCCACCTAC	120
QY	121	GGCAAGCTGAACCTGAAAGTTTCATCTGTCACCAACCGGCAAGCTGCCCGTGCCTTGGGCCACC	180
Db	121	GGCAAGCTGACCTGAAAGTTTCATCTGTCACCAACCGGCAAGCTGCCCGTGCCTTGGGCCACC	180
QY	181	CTCGTGACCAACCTGACCTACCGCGTGCAGTGCCTTCAGCGCGTACCCGACACACATGAAG	240
Db	181	CTCGTGACCAACCTGACCTACCGCGTGCAGTGCCTTCAGCGCGTACCCGACACACATGAAG	240
QY	241	CAGCACGACTTCTTCAAGTCCGCCATGCCCGGAAGGCTACGTCCAGGAGCGCACCATCTTTC	300
Db	241	CAGCACGACTTCTTCAAGTCCGCCATGCCCGGAAGGCTACGTCCAGGAGCGCACCATCTTTC	300
QY	301	TTCAAGAGCAGCGGCAACTACAGAACCCGCGCGAGGTGAAGTTCGAGGGCGACACCCCTG	360
Db	301	TTCAAGAGCAGCGGCAACTACAGAACCCGCGCGAGGTGAAGTTCGAGGGCGACACCCCTG	360
QY	361	GTGAACCGCATCGAGTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTCTGGGGCAC	420
Db	361	GTGAACCGCATCGAGTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTCTGGGGCAC	420
QY	421	AAGCTGGAGTACAACTACAAACGCCAACACGCTTATATCATGGCCGACAAAGCAGAAGAAC	480
Db	421	AAGCTGGAGTACAACTACAAACGCCAACACGCTTATATCATGGCCGACAAAGCAGAAGAAC	480
QY	481	GSCATCAAGGTGAACCTTCAAGATCCGCCAACACATCGAGCAGCGCAGCGTGCAGCTCGCC	540
Db	481	GSCATCAAGGTGAACCTTCAAGATCCGCCAACACATCGAGCAGCGCAGCGTGCAGCTCGCC	540
QY	541	GACCACTACCGACGAACACCCCATTCGGCGAGCGGCCCGTGTGTGTGCCCGACAACCCAC	600
Db	541	GACCACTACCGACGAACACCCCATTCGGCGAGCGGCCCGTGTGTGTGCCCGACAACCCAC	600
QY	601	TACCTTGACACCCAGTCCGCGCTGAGCAAGACCCCAACGAGNAAGCGCGATCACATGGTC	660
Db	601	TACCTTGACACCCAGTCCGCGCTGAGCAAGACCCCAACGAGNAAGCGCGATCACATGGTC	660
QY	661	CTGCTGGAGTTCGTGACCCGCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAGAA	719
Db	661	CTGCTGGAGTTCGTGACCCGCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTA	719

RESULT, T 13

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RES001.13
US-09-316-920A-12
; Sequence 12, Application US/09316920A
; Patent No. 6699687
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
; FILE REFERENCE: REGEN1470
; CURRENT APPLICATION NUMBER: US/09/316,920A
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Aequorea victoria
US-09-316-920A-12

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RESULT 14

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US-09-172-063-29
; Sequence 29, Application US/09172063
; Patent No. 6150176
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; APPLICANT: Llopis, Juan
; APPLICANT: Wachter, Rebekka M.
; APPLICANT: Remington, S. James
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; MEASURING THE PH OF A BIOLOGICAL SAMPLE
; FILE REFERENCE: 07257/071001
; CURRENT APPLICATION NUMBER: US/09/172,063
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 09/094,359
; EARLIER FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:

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; NAME/KEY: misc feature
; LOCATION: (0)---(0)
; OTHER INFORMATION: GT-EGFP
US-09-172-063-29

Query Match 84.4%; Score 717.4; DB 3; Length 972;
Best Local Similarity 99.9%; Pred. No. 6.9e-141;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCTGGTCAAGCTGGAC 60
Db 253 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCTGGTCAAGCTGGAC 312
QY 61 GSCGACGTAAGCGGCCACAAAGTTCAAGCTGTCCGCGAGGGCGAGGCGATGCCACCTAC 120
Db 313 GSCGACGTAAGCGGCCACAAAGTTCAAGCTGTCCGCGAGGGCGAGGCGATGCCACCTAC 372
QY 121 GGCAAGCTGACCCCTGAAAGTTTCATCTGCACACCGGCAAGCTGCCGTGCCCTGGCCACC 180
Db 373 GGCAAGCTGACCCCTGAAAGTTTCATCTGCACACCGGCAAGCTGCCGTGCCCTGGCCACC 432
QY 181 CTCGTGACACCCCTGACCTACCGGCTGAGTGTCTTACGCGCTACCCCGACCAATGAAG 240
Db 433 CTCGTGACACCCCTGACCTACCGGCTGAGTGTCTTACGCGCTACCCCGACCAATGAAG 492
QY 241 CAGCAGCACTTCTTCAAGTCCGCGATGCCGAGGCTAGTCCAGGAGCGGACCATCTTC 300
Db 493 CAGCAGCACTTCTTCAAGTCCGCGATGCCGAGGCTAGTCCAGGAGCGGACCATCTTC 552
QY 301 TTCAGGACGAGCGGCAACTCAAGACCCGCGGAGGTGAAGTTCCGAGGGCGACACCCCTG 360
Db 553 TTCAGGACGAGCGGCAACTCAAGACCCGCGGAGGTGAAGTTCCGAGGGCGACACCCCTG 612
QY 361 GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCAC 420
Db 613 GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCAC 672
QY 421 AAGCTGGAGTCAACTCAACAGCCACAACTCTATATCATGGCCGCAAGCAGAGAAC 480
Db 673 AAGCTGGAGTCAACTCAACAGCCACAACTCTATATCATGGCCGCAAGCAGAGAAC 732
QY 481 GGCATCAAGGTGAATTCAGAGTCCGCGGAGGAGCGGAGGAGCGGAGCTCGCC 540
Db 733 GGCATCAAGGTGAATTCAGAGTCCGCGGAGGAGCGGAGGAGCGGAGCTCGCC 792
QY 541 GACCACTACAGCAGAAACACCCCATCGGCGAGCGCCCGCTGCTGCCCGGACAAACC 600
Db 793 GACCACTACAGCAGAAACACCCCATCGGCGAGCGCCCGCTGCTGCCCGGACAAACC 852
QY 601 TACCTGAGCACCAGTCCGCGCTGAGCAAGACCCCAAGAGGAGCGGATCATGTGTC 660
Db 853 TACCTGAGCACCAGTCCGCGCTGAGCAAGAGCCCAAGAGGAGCGGATCATGTGTC 912
QY 661 CTGCTGGAGTTCTGAGCCGCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAGAA 719
Db 913 CTGCTGGAGTTCTGAGCCGCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTA 971
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RESULT 15

US-09-602-641-29
; Sequence 29, Application US/09602641
; Patent No. 6608189
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; APPLICANT: Llopis, Juan
; APPLICANT: Wachter, Rebekka M.
; APPLICANT: Remington, S. James
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
; FILE REFERENCE: 07257/071001
; CURRENT APPLICATION NUMBER: US/09/602,641
; CURRENT FILING DATE: 2000-06-22

; PRIOR APPLICATION NUMBER: 09/172,063
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)---(0)
; OTHER INFORMATION: GT-EGFP
US-09-602-641-29

Query Match 84.4%; Score 717.4; DB 4; Length 972;
Best Local Similarity 99.9%; Pred. No. 6.9e-141;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCTGGTCAAGCTGGAC 60
Db 253 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCTGGTCAAGCTGGAC 312
QY 61 GSCGACGTAAGCGGCCACAAAGTTCAAGCTGTCCGCGAGGGCGAGGCGATGCCACCTAC 120
Db 313 GSCGACGTAAGCGGCCACAAAGTTCAAGCTGTCCGCGAGGGCGAGGCGATGCCACCTAC 372
QY 121 GGCAAGCTGACCCCTGAAAGTTTCATCTGCACACCGGCAAGCTGCCGTGCCCTGGCCACC 180
Db 373 GGCAAGCTGACCCCTGAAAGTTTCATCTGCACACCGGCAAGCTGCCGTGCCCTGGCCACC 432
QY 181 CTCGTGACACCCCTGACCTACCGGCTGAGTGTCTTACGCGCTACCCCGACCAATGAAG 240
Db 433 CTCGTGACACCCCTGACCTACCGGCTGAGTGTCTTACGCGCTACCCCGACCAATGAAG 492
QY 241 CAGCAGCACTTCTTCAAGTCCGCGATGCCGAGGCTAGTCCAGGAGCGGACCATCTTC 300
Db 493 CAGCAGCACTTCTTCAAGTCCGCGATGCCGAGGCTAGTCCAGGAGCGGACCATCTTC 552
QY 301 TTCAGGACGAGCGGCAACTCAAGACCCGCGGAGGTGAAGTTCCGAGGGCGACACCCCTG 360
Db 553 TTCAGGACGAGCGGCAACTCAAGACCCGCGGAGGTGAAGTTCCGAGGGCGACACCCCTG 612
QY 361 GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCAC 420
Db 613 GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCAC 672
QY 421 AAGCTGGAGTCAACTCAACAGCCACAACTCTATATCATGGCCGCAAGCAGAGAAC 480
Db 673 AAGCTGGAGTCAACTCAACAGCCACAACTCTATATCATGGCCGCAAGCAGAGAAC 732
QY 481 GGCATCAAGGTGAATTCAGAGTCCGCGGAGGAGCGGAGGAGCGGAGCTCGCC 540
Db 733 GGCATCAAGGTGAATTCAGAGTCCGCGGAGGAGCGGAGGAGCGGAGCTCGCC 792
QY 541 GACCACTACAGCAGAAACACCCCATCGGCGAGCGCCCGCTGCTGCCCGGACAAACC 600
Db 793 GACCACTACAGCAGAAACACCCCATCGGCGAGCGCCCGCTGCTGCCCGGACAAACC 852
QY 601 TACCTGAGCACCAGTCCGCGCTGAGCAAGACCCCAAGAGGAGCGGATCATGTGTC 660
Db 853 TACCTGAGCACCAGTCCGCGCTGAGCAAGAGCCCAAGAGGAGCGGATCATGTGTC 912
QY 661 CTGCTGGAGTTCTGAGCCGCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAGAA 719
Db 913 CTGCTGGAGTTCTGAGCCGCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTA 971
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10/20/21

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	850	100.0	850	9	US-09-931-232-2
2	850	100.0	4336	17	US-10-679-191A-1
3	850	100.0	4862	15	US-10-161-403-87
4	845	99.4	845	17	US-10-332-733-21
5	721.2	84.8	10417	14	US-10-152-040-28
6	720.6	84.8	6418	16	US-10-408-456-2
7	720	84.7	12789	16	US-10-666-778-9
8	719.4	84.6	8255	17	US-10-334-235-17
9	719.4	84.6	8528	14	US-10-239-804-11
10	719.2	84.6	5713	9	US-09-963-206B-5
11	719.2	84.6	5713	9	US-09-966-976A-5
12	719.2	84.6	5713	12	US-09-963-247A-5

13	719	84.6	8531	15	US-10-134-643-5	Sequence 5, Appli
14	719	84.6	8531	16	US-10-408-456-1	Sequence 1, Appli
15	719	84.6	8531	16	US-10-429-608A-2	Sequence 2, Appli
16	719	84.6	8531	16	US-10-716-725-2	Sequence 2, Appli
17	718.6	84.5	1190	11	US-09-927-876-98	Sequence 98, Appl
18	718.6	84.5	1190	16	US-10-360-149-98	Sequence 98, Appl
19	718.6	84.5	1190	16	US-10-457-047-98	Sequence 98, Appl
20	718.6	84.5	1377	15	US-10-204-724-1	Sequence 1, Appli
21	718.6	84.5	4151	16	US-10-421-285-15	Sequence 15, Appli
22	718.6	84.5	4733	10	US-09-797-496B-1	Sequence 1, Appli
23	718.6	84.5	4733	15	US-10-177-390-1	Sequence 1, Appli
24	718.6	84.5	4944	13	US-10-001-189-55	Sequence 55, Appl
c	718.6	84.5	4952	13	US-10-001-189-52	Sequence 52, Appl
25	718.6	84.5	7015	9	US-09-770-315-1	Sequence 1, Appli
26	718.6	84.5	9013	13	US-10-001-189-50	Sequence 50, Appl
27	718.6	84.5	9941	14	US-10-243-553-3	Sequence 3, Appli
28	718.6	84.5	9941	14	US-10-243-816-2	Sequence 2, Appli
29	718.6	84.5	9941	15	US-10-243-820-9	Sequence 9, Appli
30	718.6	84.5	9941	15	US-10-243-817-9	Sequence 9, Appli
31	718.6	84.5	9941	15	US-10-319-341-3	Sequence 3, Appli
32	718.6	84.5	14262	17	US-10-163-863A-9	Sequence 9, Appli
33	718.6	84.5	5162	10	US-09-815-981-13	Sequence 13, Appl
34	718.2	84.5	5162	10	US-09-815-979-13	Sequence 13, Appl
35	718.2	84.5	5162	15	US-10-235-119-13	Sequence 13, Appl
36	718.2	84.5	5162	15	US-10-161-403-26	Sequence 26, Appl
37	718.2	84.5	5162	15	US-10-086-745-13	Sequence 13, Appl
38	718.2	84.5	5162	15	US-10-428-653-13	Sequence 13, Appl
39	718.2	84.5	5162	15	US-09-954-483A-14	Sequence 14, Appl
40	718	84.5	5510	15	US-10-161-403-71	Sequence 71, Appl
41	718	84.5	5510	15	US-10-473-637-9	Sequence 9, Appli
42	718	84.5	6100	15	US-10-314-861-36	Sequence 36, Appl
43	718	84.5	6115	15	US-10-314-861-34	Sequence 34, Appl
44	718	84.5	6119	15	US-10-161-403-126	Sequence 126, App
c	718	84.5	6119	15		

ALIGNMENTS

RESULT 1
US-09-931-232-2
; Sequence 2, Application US/09931232
; Publication No. US20020058274A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xianqiang
; TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins
; FILE REFERENCE: CLON075CON
; CURRENT APPLICATION NUMBER: US/09/931.232
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/364,946
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/191,233
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 09/062,102
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 60/060,855
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 850
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of the EGFP-MODC422_461 fusion protein.
US-09-931-232-2

Query Match 100.0%; Score 850; DB 9; Length 850;
Best Local Similarity 100.0%; Pred. No. 7.4e-189;
Matches 850; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1	ATGCTGAGCAAGGGCGAGGAGCTGTTTCA	CGGGGTGGTGCCCATCTCGTTCAGCTGGAC	60
1	ATGCTGAGCAAGGGCGAGGAGCTGTTTCA	CGGGGTGGTGCCCATCTCGTTCAGCTGGAC	60
61	GGCGACGTAAACCGGCCCAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTTAC	120	
61	GGCGACGTAAACCGGCCCAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTTAC	120	
121	GGCAAGCTGACCTGAAGTTCATCTGCACACCGGCAAGCTGCCGTGCTTGGCCCTGGCCACC	180	
121	GGCAAGCTGACCTGAAGTTCATCTGCACACCGGCAAGCTGCCGTGCTTGGCCCTGGCCACC	180	
181	CTCGTGACCAACCTTGACTACGCGGTGAGTCTTCAGCCGCTTACCCGACCACTGAAG	240	
181	CTCGTGACCAACCTTGACTACGCGGTGAGTCTTCAGCCGCTTACCCGACCACTGAAG	240	
241	CAGCAAGCTTCTTCAAGTCCGGCATGCCGAAGGCTACGTCCAGGAGCGCAATCTTC	300	
241	CAGCAAGCTTCTTCAAGTCCGGCATGCCGAAGGCTACGTCCAGGAGCGCAATCTTC	300	
301	TTCAAGGACGACGGCAACTCAAGACCGCGCGCGAGTGAAGTTCGAGGGCGACACCTTG	360	
301	TTCAAGGACGACGGCAACTCAAGACCGCGCGCGAGTGAAGTTCGAGGGCGACACCTTG	360	
361	GTGAACCGCATCGAGTGAAGGGGATCGACTTCGAGGAGCGGGCAACTTCCTGGGGCAC	420	
361	GTGAACCGCATCGAGTGAAGGGGATCGACTTCGAGGAGCGGGCAACTTCCTGGGGCAC	420	
421	RAGCTGGAGTCAACTCAACAGCCAAAGTCTATATCATGGCCGACAGCAGAAGAAC	480	
421	RAGCTGGAGTCAACTCAACAGCCAAAGTCTATATCATGGCCGACAGCAGAAGAAC	480	
481	GGCATCAAGGTGAATTCAGATCCGCCCAACATCGAGGACGGGAGCGTGAAGCTCGCC	540	
481	GGCATCAAGGTGAATTCAGATCCGCCCAACATCGAGGACGGGAGCGTGAAGCTCGCC	540	
541	GACCACTACGACGACACCCCATCGGGAGCGCCCGTGTCTGTCGCCGACCAACCAC	600	
541	GACCACTACGACGACACCCCATCGGGAGCGCCCGTGTCTGTCGCCGACCAACCAC	600	
601	TACCTGAGCACCCAGTCCGCCCTGAGCAAAAGACCCCAACGAGAGCGGATCATGGTCT	660	
601	TACCTGAGCACCCAGTCCGCCCTGAGCAAAAGACCCCAACGAGAGCGGATCATGGTCT	660	
661	CTGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGGCATGACGAGCTGTACAGAGAG	720	
661	CTGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGGCATGACGAGCTGTACAGAGAG	720	
721	CTTAGCATGGCTTCCCGCGGAGTGGAGGACGAGTATGSCACGCTGCCCATGTCT	780	
721	CTTAGCATGGCTTCCCGCGGAGTGGAGGACGAGTATGSCACGCTGCCCATGTCT	780	
781	TGTGCCAGGAGCGGGATGAGCGGTCAACCTCGAGCTGTGCTTCTGCTAGATCAAT	840	
781	TGTGCCAGGAGCGGGATGAGCGGTCAACCTCGAGCTGTGCTTCTGCTAGATCAAT	840	
841	GTGTAGATGC	850	
841	GTGTAGATGC	850	

RESULT 2
 US-10-679-191A-1
 Sequence 1, Application US/10679191A
 Publication No. US20040168210A1
 GENERAL INFORMATION:
 APPLICANT: Moon, Randall T.
 APPLICANT: Dorsky, Richard I.
 TITLE OF INVENTION: Transgenic Fish and Beta-Catenin Signaling Pathway Model
 FILE REFERENCE: UWOT121818
 CURRENT APPLICATION NUMBER: US/10/679,191A
 CURRENT FILING DATE: 2003-10-03
 CONFIDENTIALITY: 504

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Db 4085 TACCTGAGCACCCAGTCCGCTGAGCAGAGACCCCAACGAGAGCGCGATCACATGGTC 4144
QY 661 CTGCTGGAGTTCTGAGCCGCGCGGGATCACTTCGGGATGGAAGAGCTGTACAGAG 720
Db 4145 CTGCTGGAGTTCTGAGCCGCGCGGGATCACTTCGGGATGGAAGAGCTGTACAGAG 4204
QY 721 CTTAGCCATGGCTTCCCGCGAGGTGGAGGAGCAGGATGAGGACGCTGCCATGCT 780
Db 4205 CTTAGCCATGGCTTCCCGCGAGGTGGAGGAGCAGGATGAGGACGCTGCCATGCT 4264
QY 781 TGTGCCAGGAGCGGGATGACCGTCAACCTGCGAGCGCTGTGCTTCTAGGATCAAT 840
Db 4265 TGTGCCAGGAGCGGGATGACCGTCAACCTGCGAGCGCTGTGCTTCTAGGATCAAT 4324
QY 841 GTGTAGATGC 850
Db 4325 GTGTAGATGC 4334

RESULT 3
US-10-161-403-87
; Sequence 87, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 4862
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pd2egfp-1N plasmid from Clontech
US-10-161-403-87

Query Match 100.0%; Score 850; DB 15; Length 4862;
Best Local Similarity 100.0%; Pred. No. 8.3e-189;
Matches 850; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGTGTGCCATCCCTGGTCTGAGCTGGAC 60
Db 679 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGTGTGCCATCCCTGGTCTGAGCTGGAC 738
QY 61 GGGAGCGTAAACGGGCCCAAGTTAGCGTGTCCGGCGAGGGCGAGGCGGATGCCACCTAC 120
Db 739 GGGAGCGTAAACGGGCCCAAGTTAGCGTGTCCGGCGAGGGCGAGGCGGATGCCACCTAC 798
QY 121 GGCAAGCTGACCTGAGTTTCATCTGCACCAACCGGGAAGCTGCCGTGCCCTGGCCCAACC 180
Db 799 GGCAAGCTGACCTGAGTTTCATCTGCACCAACCGGGAAGCTGCCGTGCCCTGGCCCAACC 858
QY 181 CTGCTGACCAACCTGACCTACGGCGTGCAGTGTTCAGCCGCTACCCCGACCATCAAG 240
Db 859 CTGCTGACCAACCTGACCTACGGCGTGCAGTGTTCAGCCGCTACCCCGACCATCAAG 918
QY 241 CAGCAGACTTCTTCAAGTCCCGCATGCCCGAAGGCTACGTCAGGAGCGGCACCATCTTC 300
Db 919 CAGCAGACTTCTTCAAGTCCCGCATGCCCGAAGGCTACGTCAGGAGCGGCACCATCTTC 978
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QY 301 TTCAAGGAGCAGCGGCAACTACAAGACCCCGCGGAGGTGAAGTTTCAGGGCGGACACCTTG 360
Db 979 TTCAAGGAGCAGCGGCAACTACAAGACCCCGCGGAGGTGAAGTTTCAGGGCGGACACCTTG 1038
QY 361 GTGAACCGCATCGAGCTGAAGGGCATTCGACTTCAAGGAGCAGCGCAACATCTCTGGGGCAC 420
Db 1039 GTGAACCGCATCGAGCTGAAGGGCATTCGACTTCAAGGAGCAGCGCAACATCTCTGGGGCAC 1098
QY 421 AAGCTGGAGTCAACTACAAGACCCCGGACACGCTTATATATCATGCGCGACAAGCAGAAGAC 480
Db 1099 AAGCTGGAGTCAACTACAAGACCCCGGACACGCTTATATATCATGCGCGACAAGCAGAAGAC 1158
QY 481 GGCATCAAGGGTGAACCTTCAAGATCCGCCCAACAACATCGAGGACGCGAGCTGCAGCTCGCC 540
Db 1159 GGCATCAAGGGTGAACCTTCAAGATCCGCCCAACAACATCGAGGACGCGAGCTGCAGCTCGCC 1218
QY 541 GACCACTACGAGCAACACACCCCATCGGCGAGCGGCCCGCTGCTGCTGCCGACCAACAC 600
Db 1219 GACCACTACGAGCAACACACCCCATCGGCGAGCGGCCCGCTGCTGCTGCCGACCAACAC 1278
QY 601 TACCTGAGCACCAGTCCGCTCGAGCAAGACCCCAAGAGAGAGAGGCGGATCAGTCTGC 660
Db 1279 TACCTGAGCACCAGTCCGCTCGAGCAAGAGAGAGAGAGGCGGATCAGTCTGC 1338
QY 661 CTGCTGGAGTTCTGTAACCGCGCGGGATCACTCTCGGCATGGACGAGCTGTACAGAAG 720
Db 1339 CTGCTGGAGTTCTGTAACCGCGCGGGATCACTCTCGGCATGGACGAGCTGTACAGAAG 1398
QY 721 CTTAGCCATGGCTTCCCGCGGAGGTGGAGGAGGATGATGGCACGCTGCCCATGCT 780
Db 1399 CTTAGCCATGGCTTCCCGCGGAGGTGGAGGAGGATGATGGCACGCTGCCCATGCT 1458
QY 781 TGTGCCAGGAGAGCGGATGAGCGCTCAACCTCGAGCTGCTTCTGCTAGGATCAAT 840
Db 1459 TGTGCCAGGAGAGCGGATGAGCGCTCAACCTCGAGCTGCTTCTGCTAGGATCAAT 1518
QY 841 GTGTAGATGC 850
Db 1519 GTGTAGATGC 1528

RESULT 4
US-10-332-733-21
; Sequence 21, Application US/10332733
; Publication No. US20040106565A1
; GENERAL INFORMATION:
; APPLICANT: Margaret Odenthal and Diana Jung
; TITLE OF INVENTION: Gene Expression, Genome Alteration And Reporter Expression
; FILE REFERENCE: In Myofibroblasts And Myofibroblast-like Cells
; CURRENT APPLICATION NUMBER: US/10/332,733
; CURRENT FILING DATE: 2003-06-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 21
; LENGTH: 845
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: EGFP
US-10-332-733-21

Query Match 99.4%; Score 845; DB 17; Length 845;
Best Local Similarity 100.0%; Pred. No. 1.1e-187;
Matches 845; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGTGTGCCATCTCTGGTCTGAGCTGGAC 60
Db 1 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGTGTGCCATCTCTGGTCTGAGCTGGAC 60
QY 61 GGGAGCGTAAACGGGCCCAAGTTAGCGTGTCCGGCGAGGGCGAGGCGGATGCCACCTAC 120
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APPLICANT: KINGSMAN, et al., Alan John
; TITLE OF INVENTION: Vector System
; FILE REFERENCE: 674523-2016
; CURRENT APPLICATION NUMBER: US/10/408,456
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/04433
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0024550.6
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 6418
; TYPE: DNA
; ORGANISM: Equine Infectious Anemia Virus
US-10-408-456-2

Query Match 84.8%; Score 720.6; DB 16; Length 6418;
Best Local Similarity 96.8%; Pred. No. 1.3e-158;
Matches 735; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 ATGGTGAGCAAGGGCGAGGAGTGTTCACCGGGGTGGTCCCATCTCTGTCGAGCTGGAC 60
Db |||||
QY 2690 ATGGTGAGCAAGGGCGAGGAGTGTTCACCGGGGTGGTCCCATCTCTGTCGAGCTGGAC 2749
Db |||||
QY 61 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCGGGAGGGCGAGGCGATGCCACCTAC 120
Db |||||
QY 2750 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCGGGAGGGCGAGGCGATGCCACCTAC 2809
Db |||||
QY 121 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCGGGAGGGCGAGGCGATGCCACCTAC 180
Db |||||
QY 2810 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCGGGAGGGCGAGGCGATGCCACCTAC 2869
Db |||||
QY 181 CTCGTGACACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 240
Db |||||
QY 2870 CTCGTGACACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 2929
Db |||||
QY 241 CAGCAGCACTTCTTCAAGTCGCGCATGCGCGAGGAGTTCAGCGTGTCCGGGAGGGCGAGGCG 300
Db |||||
QY 2930 CAGCAGCACTTCTTCAAGTCGCGCATGCGCGAGGAGTTCAGCGTGTCCGGGAGGGCGAGGCG 2989
Db |||||
QY 301 TTCAGGACGACGGCAACTACAAAGACCGCGCGAGGAGTTCAGCGTGTCCGGGAGGGCGAGGCG 360
Db |||||
QY 2990 TTCAGGACGACGGCAACTACAAAGACCGCGCGAGGAGTTCAGCGTGTCCGGGAGGGCGAGGCG 3049
Db |||||
QY 361 GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTCTGGGGCAC 420
Db |||||
QY 3050 GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTCTGGGGCAC 3109
Db |||||
QY 421 AAGCTGGAGTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACT 480
Db |||||
QY 3110 AAGCTGGAGTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACT 3169
Db |||||
QY 481 GGCACTAAGGTGAATCTTCAAGTCCGCGCAACAACTCGAGGACGGCAGCGTCACTCGCC 540
Db |||||
QY 3170 GGCACTAAGGTGAATCTTCAAGTCCGCGCAACAACTCGAGGACGGCAGCGTCACTCGCC 3229
Db |||||
QY 541 GACCACTACAGGAGAACACCCCATCGGCGACGGCCCGGTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db |||||
QY 3230 GACCACTACAGGAGAACACCCCATCGGCGACGGCCCGGTGCTGCTGCTGCTGCTGCTGCTGCT 3289
Db |||||
QY 601 TACCTGAGCACCAGTCCGCGCTGAGCAGAACAGACCCCAAGAGAGCGGATCACTGGTC 660
Db |||||
QY 3290 TACCTGAGCACCAGTCCGCGCTGAGCAGAACAGACCCCAAGAGAGCGGATCACTGGTC 3349
Db |||||
QY 661 CTGCTGGAGTTCGTGACCGCGCGCGGATCACTCTCGGCATGGAGCAGCTGTACAAGAG 720
Db |||||
QY 3350 CTGCTGGAGTTCGTGACCGCGCGCGGATCACTCTCGGCATGGAGCAGCTGTACAAGAG 720
Db |||||
QY 721 CTGAGCAGTGGCTTCCGCGCGGAGGTGGAGGAGGAGT 759
Db |||||
QY 3410 AGCGCGCGGAGTCTAGAGTCTGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCT 3448
Db |||||

RESULT 7

US-10-666-778-9/c
; Sequence 9, Application US/10666778
; Publication No. US20040064849A1
; GENERAL INFORMATION:
; APPLICANT: Goossens, Alain
; APPLICANT: Inze, Dirk
; TITLE OF INVENTION: THE USE OF GENES ENCODING MEMBRANE TRANSPORTER PUMPS TO STIMULATE PRODUCTION OF SECONDARY METABOLITES IN BIOLOGICAL CELLS
; FILE REFERENCE: DI/ABC/V082
; CURRENT APPLICATION NUMBER: US/10/666,778
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: EP01201407.2
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 12789
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vector pK7WG2D
; NAME/KEY: misc feature
; LOCATION: (4772)..(4772)
; OTHER INFORMATION: n can be any base
US-10-666-778-9

Query Match 84.7%; Score 720; DB 16; Length 12789;
Best Local Similarity 100.0%; Pred. No. 1.9e-158;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGACCAAGGGCGAGGAGTGTTCACCGGGGTGGTCCCATCTCTGTCGAGCTGGAC 60
Db |||||
QY 5797 ATGGTGACCAAGGGCGAGGAGTGTTCACCGGGGTGGTCCCATCTCTGTCGAGCTGGAC 5738
Db |||||
QY 61 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCGGGAGGGCGAGGCGATGCCACCTAC 120
Db |||||
QY 5737 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCGGGAGGGCGAGGCGATGCCACCTAC 5678
Db |||||
QY 121 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCGGGAGGGCGAGGCGATGCCACCTAC 180
Db |||||
QY 5677 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCGGGAGGGCGAGGCGATGCCACCTAC 5618
Db |||||
QY 181 CTCGTGACACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 240
Db |||||
QY 5617 CTCGTGACACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 5558
Db |||||
QY 241 CAGCAGCACTTCTTCAAGTCCGCCATGCCGAAAGCTACGTCCAGGAGCGCACCATCTTC 300
Db |||||
QY 5557 CAGCAGCACTTCTTCAAGTCCGCCATGCCGAAAGCTACGTCCAGGAGCGCACCATCTTC 5498
Db |||||
QY 301 TTCAAGGACGACGGCAACTCAAGACCCCGCGCCGAGTGAAGTTCGAGGGCGACACCCCTG 360
Db |||||
QY 5497 TTCAAGGACGACGGCAACTCAAGACCCCGCGCCGAGTGAAGTTCGAGGGCGACACCCCTG 5438
Db |||||
QY 361 GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTCTGGGGCAC 420
Db |||||
QY 5437 GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTCTGGGGCAC 5378
Db |||||
QY 421 AAGCTGGAGTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACT 480
Db |||||
QY 5377 AAGCTGGAGTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACT 5318
Db |||||
QY 481 GGCACTAAGGTGAATCTTCAAGTCCGCGCAACAACTCGAGGACGGCAGCTGTCAAGAG 540
Db |||||
QY 5317 GGCACTAAGGTGAATCTTCAAGTCCGCGCAACAACTCGAGGACGGCAGCTGTCAAGAG 5258
Db |||||
QY 541 GACCACTTACAGCAGAACACCCCATCGGCGAGGGCCCGGTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db |||||
QY 5257 GACCACTTACAGCAGAACACCCCATCGGCGAGGGCCCGGTGCTGCTGCTGCTGCTGCTGCTGCT 5198
Db |||||

QY	601	TACCTGAGCACCAGTCCGCTCGCTGAGCAAGACCCCAAGCAGAGCGCGATCACATGTC	660
Db	5197	TACCTGAGCACCAGTCCGCTCGCTGAGCAAGACCCCAAGCAGAGCGCGATCACATGTC	5138
QY	661	CTGCTGGAGTTCGTGACCGCCCGGGATCACTCTCGGCATCGACGAGCTGTACAAGAG	720
Db	5137	CTGCTGGAGTTCGTGACCGCCCGGGATCACTCTCGGCATCGACGAGCTGTACAAGAG	5078
RESULT 8			
US-10-334-235-17			
; Sequence 17, Application US/10334235			
; Publication No. US20040131591A1			
; GENERAL INFORMATION:			
; APPLICANT: Kingsman, Alan			
; APPLICANT: Kingsman, Christopher			
; APPLICANT: Bebbington, Miles			
; APPLICANT: Carroll, Fiona			
; APPLICANT: Ellard, Susan			
; APPLICANT: Myers, Kevin			
; APPLICANT: Lamikandra, Abigail			
; TITLE OF INVENTION: VECTOR SYSTEM			
; FILE REFERENCE: 53268200920			
; CURRENT APPLICATION NUMBER: US/10/334,235			
; CURRENT FILING DATE: 2002-12-30			
; PRIOR APPLICATION NUMBER: US 10/060,585			
; PRIOR FILING DATE: 2002-01-29			
; PRIOR APPLICATION NUMBER: PCT/GB00/04317			
; PRIOR FILING DATE: 2000-11-13			
; PRIOR APPLICATION NUMBER: US 09/445,375			
; PRIOR FILING DATE: 1998-06-04			
; NUMBER OF SEQ ID NOS: 40			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 17			
; LENGTH: 8255			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: nuc sequence of the SMART2G5' cPPT plasmid			
US-10-334-235-17			
Query Match 84.6%; Score 719.4; DB 17; Length 8255;			
Best Local Similarity 97.2%; Pred. No. 2.6e-158;			
Matches 732; Conservative 0; Mismatches 21; Indels 0; Gaps 0;			
QY	1	ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGTGCGCATCTCTGTGCGAGCTGGAC	60
Db	2868	ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGTGCGCATCTCTGTGCGAGCTGGAC	2927
QY	61	GGCGAGCTAAACGGCCCAAGATTTCAGCGGTGTCGGCGAGGGCGAGGCGGATGCCACCTAC	120
Db	2928	GGCGAGCTAAACGGCCCAAGATTTCAGCGGTGTCGGCGAGGGCGAGGCGGATGCCACCTAC	2987
QY	121	GGCGAGCTAAACGGCCCAAGATTTCAGCGGTGTCGGCGAGGGCGAGGCGGATGCCACCTAC	180
Db	2988	GGCGAGCTAAACGGCCCAAGATTTCAGCGGTGTCGGCGAGGGCGAGGCGGATGCCACCTAC	3047
QY	181	CTCGTGACCAACCTGACCTGAGTTCATCTGACCGGGGTGTGCGCATCTCTGTGCGAGCTGGAC	240
Db	3048	CTCGTGACCAACCTGACCTGAGTTCATCTGACCGGGGTGTGCGCATCTCTGTGCGAGCTGGAC	3107
QY	241	CAGCAGCACTTCTTCAAGTCCGCTGACCTGAGTTCATCTGACCGGGGTGTGCGCATCTCTGTGCGAGCTGGAC	300
Db	3108	CAGCAGCACTTCTTCAAGTCCGCTGACCTGAGTTCATCTGACCGGGGTGTGCGCATCTCTGTGCGAGCTGGAC	3167
QY	301	TTCAAGGACGAGCGCAACTCAAGACCGCGCGAGGTGAAATTTCGAGGGCGACACCTG	360
Db	3168	TTCAAGGACGAGCGCAACTCAAGACCGCGCGAGGTGAAATTTCGAGGGCGACACCTG	3227
QY	361	GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGAGGAGCGGCAACATCTGCGGGGAC	420
Db	3228	GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGAGGAGCGGCAACATCTGCGGGGAC	3287

QY	421	AAGCTGGAGTACAACTACAAAGCCCAACAGCTCTATATCATGGCCGCAAGCAGAAGAAC	480
Db	3288	AAGCTGGAGTACAACTACAAAGCCCAACAGCTCTATATCATGGCCGCAAGCAGAAGAAC	3347
QY	481	GGCATCAAGGTGAACCTTCAAGATCCGCCCAACATCGAGGAGCGGCGATGCGCTCGCC	540
Db	3348	GGCATCAAGGTGAACCTTCAAGATCCGCCCAACATCGAGGAGCGGCGATGCGCTCGCC	3407
QY	541	GACCACTACAGCAGAACACCCCGCATCGGAGCGGCCCGTGTCTGCTGCCGCAACACAC	600
Db	3408	GACCACTACAGCAGAACACCCCGCATCGGAGCGGCCCGTGTCTGCTGCCGCAACACAC	3467
QY	601	TACCTGAGCACCAGTCCGCCCTGAGCAAGACCCCAACAGGAGCGCGATCACATGTC	660
Db	3468	TACCTGAGCACCAGTCCGCCCTGAGCAAGACCCCAACAGGAGCGCGATCACATGTC	3527
QY	661	CTGCTGGAGTTCGTGACCGCCCGGGATCACTCTCGGCATGAGCAGCTGTACAAGAG	720
Db	3528	CTGCTGGAGTTCGTGACCGCCCGGGATCACTCTCGGCATGAGCAGCTGTACAAGAG	3587
QY	721	CTTAGCATGGCTTCCCGCGGAGGTGGAGGAG	753
Db	3588	AGCGCGCGGACTCTAGATCGACCTCGAGGGG	3620
RESULT 9			
US-10-239-804-11			
; Sequence 11, Application US/10239804			
; Publication No. US20030053991A1			
; GENERAL INFORMATION:			
; APPLICANT: Oxford Biomedica (UK) Limited			
; APPLICANT: Kingsman, Alan J			
; APPLICANT: Maden, Malcolm			
; APPLICANT: Corcoran, Jonathan PT			
; TITLE OF INVENTION: Factor			
; FILE REFERENCE: P009156WOCTH			
; CURRENT APPLICATION NUMBER: US/10/239,804			
; CURRENT FILING DATE: 2002-09-23			
; PRIOR APPLICATION NUMBER: PCT/GB00/01211			
; PRIOR FILING DATE: 2000-03-30			
; PRIOR APPLICATION NUMBER: GB 0024300.6			
; PRIOR FILING DATE: 2000-10-04			
; NUMBER OF SEQ ID NOS: 73			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 11			
; LENGTH: 8528			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: PONY8G 5'cPPT			
; OTHER INFORMATION: POS delCTS EIAV vector genome plasmid			
US-10-239-804-11			
Query Match 84.6%; Score 719.4; DB 14; Length 8528;			
Best Local Similarity 97.2%; Pred. No. 2.6e-158;			
Matches 732; Conservative 0; Mismatches 21; Indels 0; Gaps 0;			
QY	1	ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGTGCGCATCTCTGTGCGAGCTGGAC	60
Db	2868	ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGTGCGCATCTCTGTGCGAGCTGGAC	2927
QY	61	GGCGAGCTAAACGGCCCAAGATTTCAGCGGTGTCGGCGAGGGCGAGGCGGATGCCACCTAC	120
Db	2928	GGCGAGCTAAACGGCCCAAGATTTCAGCGGTGTCGGCGAGGGCGAGGCGGATGCCACCTAC	2987
QY	121	GGCGAGCTAAACGGCCCAAGATTTCAGCGGTGTCGGCGAGGGCGAGGCGGATGCCACCTAC	180
Db	2988	GGCGAGCTAAACGGCCCAAGATTTCAGCGGTGTCGGCGAGGGCGAGGCGGATGCCACCTAC	3047
QY	181	CTCGTGACCAACCTGACCTGAGTTCATCTGACCGGGGTGTGCGCATCTCTGTGCGAGCTGGAC	240
Db	3048	CTCGTGACCAACCTGACCTGAGTTCATCTGACCGGGGTGTGCGCATCTCTGTGCGAGCTGGAC	3107

QY 241 CAGCAGCACTTCTTCAAGTCCGCAATGCCGGAAGGCTAGCTCCAGAGGCGACCAATCTTC 300
Db 3108 CAGCAGCACTTCTTCAAGTCCGCAATGCCGGAAGGCTAGCTCCAGAGGCGACCAATCTTC 3167
QY 301 TTCAAGGACGAGCGGCAACTACAAGACCCGCGCGAGGTGAAGTTTCAGGGCGACACCCCTG 3227
Db 3168 TTCAAGGACGAGCGGCAACTACAAGACCCGCGCGAGGTGAAGTTTCAGGGCGACACCCCTG 3227
QY 361 GTGAACCGGATCGAGCTGAAGGCGATCGACTTCAAGAGGAGCGGCAACATCTCTGGGGCAC 420
Db 3228 GTGAACCGGATCGAGCTGAAGGCGATCGACTTCAAGAGGAGCGGCAACATCTCTGGGGCAC 3287
QY 421 AAGCTGGAGTCAACTACAAGGCGACACACCTGTATATCATGCGCGACAGCAGAGAAC 480
Db 3288 AAGCTGGAGTCAACTACAAGGCGACACACCTGTATATCATGCGCGACAGCAGAGAAC 3347
QY 481 GGCATCAAGGTGAATCTTCAAGATCCGCCCAACATCGAGGAGCGGAGCTCGCC 540
Db 3348 GGCATCAAGGTGAATCTTCAAGATCCGCCCAACATCGAGGAGCGGAGCTCGCC 3407
QY 541 GACCACTACGAGCAAGCAACCCCGATCGCGGAGCGGCGGCTCTCTCCCGACCAACCAC 600
Db 3408 GACCACTACGAGCAAGCAACCCCGATCGCGGAGCGGCGGCTCTCTCCCGACCAACCAC 3467
QY 601 TACCTGAGCACCAGCTCGCGCTGAGCAAGACCCCAAGAGAGCGGATCAGATGTC 660
Db 3468 TACCTGAGCACCAGCTCGCGCTGAGCAAGACCCCAAGAGAGCGGATCAGATGTC 3527
QY 661 CTGCTGGAGTTCGTGACCGCGCGCGGATCACTCTCGGATGAGAGCTGTACAGAGAG 720
Db 3528 CTGCTGGAGTTCGTGACCGCGCGCGGATCACTCTCGGATGAGAGCTGTACAGAGAG 3587
QY 721 CTTAGCCATGGCTCCCGCGGAGGTGAGGAG 753
Db 3588 AGCGCGCGGACTCTAGATCGACCTCGAGGGG 3620

RESULT 10

US-09-963-206B-5
; Sequence 5, Application US/09963206B
; Patent No. US20020123076A1
; GENERAL INFORMATION:
; APPLICANT: Perrick, David A.
; APPLICANT: Swift, Susan E.
; APPLICANT: Armstrong, Randall
; APPLICANT: Fox, Bryan
; TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige Syn
; FILE REFERENCE: A-66038-3/RMS/JJD/DLR
; CURRENT APPLICATION NUMBER: US/09/963,206B
; CURRENT FILING DATE: 2001-09-25
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5713
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-963-206B-5

Query Match 84.6%; Score 719.2; DB 9; Length 5713;
Best Local Similarity 98.9%; Pred. No. 2.8e-158;
Matches 724; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGTGGTGGCCATCTCGTGTGAGCTGAC 60
Db 2150 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGTGGTGGCCATCTCGTGTGAGCTGAC 2209
QY 61 GGCACGCTAAACGCCACCAAGTTTCAGCTGTCCGCGAGGGCGGAGGCGATGCCACCTAC 120

Db 2210 GCGCAGCTAAACGCCACCAAGTTTCAGCTGTCCGCGAGGGCGAGGCGATGCCACCTAC 2269
QY 121 GCGCAGCTGACCTCAAGTTTCATCTGCAACCGCAAGCTGCCGTGCCCTGGCCACCC 180
Db 2270 GCGCAGCTGACCTCAAGTTTCATCTGCAACCGCAAGCTGCCGTGCCCTGGCCACCC 2329
QY 181 CTCGTGACACCCCTGACCTGAGCGCTGAGTCTTTCAGCGCTACCCCGACCAATGAAG 240
Db 2330 CTCGTGACACCCCTGACCTGAGCGCTGAGTCTTTCAGCGCTACCCCGACCAATGAAG 2389
QY 241 CAGCAGCACTTCTTCAAGTCCGCGATGCCGAGGCTAGCTCCAGAGGCGACCACTTTC 300
Db 2390 CAGCAGCACTTCTTCAAGTCCGCGATGCCGAGGCTAGCTCCAGAGGCGACCACTTTC 2449
QY 301 TTCAAGGACGAGCGGCAACTACAAGACCCGCGCGAGGTGAAGTTTCAGGGCGACACCCCTG 360
Db 2450 TTCAAGGACGAGCGGCAACTACAAGACCCGCGCGAGGTGAAGTTTCAGGGCGACACCCCTG 2509
QY 361 GTGAACCGGATCGAGCTGAAGGCGATCGACTTCAAGAGGAGCGGCAACATCTCTGGGGCAC 420
Db 2510 GTGAACCGGATCGAGCTGAAGGCGATCGACTTCAAGAGGAGCGGCAACATCTCTGGGGCAC 2569
QY 421 AAGCTGGAGTCAACTACAAGGCGACACACCTGTATATCATGCGCGACAGCAGAGAAC 480
Db 2570 AAGCTGGAGTCAACTACAAGGCGACACACCTGTATATCATGCGCGACAGCAGAGAAC 2629
QY 481 GGCATCAAGGTGAATCTTCAAGATCCGCCCAACATCGAGGAGCGGAGCTCGCTCGCC 540
Db 2630 GGCATCAAGGTGAATCTTCAAGATCCGCCCAACATCGAGGAGCGGAGCTCGCTCGCC 2689
QY 541 GACCACTACGAGCAAGCAACCCCGATCGCGGAGCGGCGGCTCTCTCCCGACCAACCAC 600
Db 2690 GACCACTACGAGCAAGCAACCCCGATCGCGGAGCGGCGGCTCTCTCCCGACCAACCAC 2749
QY 601 TACCTGAGCACCAGCTCGCGCTGAGCAAGACCCCAAGAGAGCGGATCAGATGTC 660
Db 2750 TACCTGAGCACCAGCTCGCGCTGAGCAAGACCCCAAGAGAGCGGATCAGATGTC 2809
QY 661 CTGCTGGAGTTCGTGACCGCGCGCGGATCACTCTCGGATGAGAGCTGTACAGAGAG 720
Db 2810 CTGCTGGAGTTCGTGACCGCGCGCGGATCACTCTCGGATGAGAGCTGTACAGAGAG 2869
QY 721 CTTAGCCATGGC 732
Db 2870 TTCGAGGTGGC 2881

RESULT 11

US-09-966-976A-5
; Sequence 5, Application US/09966976A
; Patent No. US20020168649A1
; GENERAL INFORMATION:
; APPLICANT: Perrick, David A.
; APPLICANT: Swift, Susan E.
; APPLICANT: Armstrong, Randall
; APPLICANT: Fox, Bryan
; TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige Syn
; FILE REFERENCE: A-66038-4/RMS/JJD/DLR
; CURRENT APPLICATION NUMBER: US/09/966,976A
; CURRENT FILING DATE: 2001-09-27
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5713
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-966-976A-5

Query Match 84.6%; Score 719.2; DB 9; Length 5713;
Best Local Similarity 98.9%; Pred. No. 2.8e-158;
Matches 724; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
1 ATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGGTGGTCCCATCTCTGGTCGAGCTGGAC 60
2150 ATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGGTGGTCCCATCTCTGGTCGAGCTGGAC 2209
61 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 120
2210 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 2269
121 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 180
2270 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 2329
181 CTGCTGACCAACCGCTGACCTACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 240
2330 CTGCTGACCAACCGCTGACCTACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2389
241 CAGCAGACTTCTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 300
2390 CAGCAGACTTCTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2449
301 TTCAAGGACGAGCGCAACTACAAAGCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 360
2450 TTCAAGGACGAGCGCAACTACAAAGCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2509
361 GTGAACCGCATCCGATCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 420
2510 GTGAACCGCATCCGATCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2569
421 AAGCTGGAGTACAACTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 480
2570 AAGCTGGAGTACAACTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2629
481 GGCATCAAGGTGAAGTTCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 540
2630 GGCATCAAGGTGAAGTTCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2689
541 GACCACTACGAGCAAGCAACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 600
2690 GACCACTACGAGCAAGCAACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2749
721 CTAGCCATGGC 732
2870 TTGGAGGTGGC 2881

Query Match 84.6%; Score 719.2; DB 12; Length 5713;
Best Local Similarity 98.9%; Pred. No. 2.8e-158;
Matches 724; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
1 ATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGGTGGTCCCATCTCTGGTCGAGCTGGAC 60
2150 ATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGGTGGTCCCATCTCTGGTCGAGCTGGAC 2209
61 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 120
2210 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 2269
121 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 180
2270 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 2329
181 CTGCTGACCAACCGCTGACCTACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 240
2330 CTGCTGACCAACCGCTGACCTACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2389
241 CAGCAGACTTCTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 300
2390 CAGCAGACTTCTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2449
301 TTCAAGGACGAGCGCAACTACAAAGCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 360
2450 TTCAAGGACGAGCGCAACTACAAAGCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2509
361 GTGAACCGCATCCGATCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 420
2510 GTGAACCGCATCCGATCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2569
421 AAGCTGGAGTACAACTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 480
2570 AAGCTGGAGTACAACTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2629
481 GGCATCAAGGTGAAGTTCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 540
2630 GGCATCAAGGTGAAGTTCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2689
541 GACCACTACGAGCAAGCAACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 600
2690 GACCACTACGAGCAAGCAACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2749
721 CTAGCCATGGC 732
2870 TTGGAGGTGGC 2881

PRIOR FILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent in version 3.1
SEQ ID NO 5
LENGTH: 5713
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-09-963-247A-5

Query Match 84.6%; Score 719.2; DB 9; Length 5713;
Best Local Similarity 98.9%; Pred. No. 2.8e-158;
Matches 724; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
1 ATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGGTGGTCCCATCTCTGGTCGAGCTGGAC 60
2150 ATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGGTGGTCCCATCTCTGGTCGAGCTGGAC 2209
61 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 120
2210 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 2269
121 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 180
2270 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 2329
181 CTGCTGACCAACCGCTGACCTACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 240
2330 CTGCTGACCAACCGCTGACCTACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2389
241 CAGCAGACTTCTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 300
2390 CAGCAGACTTCTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2449
301 TTCAAGGACGAGCGCAACTACAAAGCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 360
2450 TTCAAGGACGAGCGCAACTACAAAGCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2509
361 GTGAACCGCATCCGATCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 420
2510 GTGAACCGCATCCGATCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2569
421 AAGCTGGAGTACAACTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 480
2570 AAGCTGGAGTACAACTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2629
481 GGCATCAAGGTGAAGTTCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 540
2630 GGCATCAAGGTGAAGTTCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2689
541 GACCACTACGAGCAAGCAACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 600
2690 GACCACTACGAGCAAGCAACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2749
601 TACCTGAGCACCAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 660
2750 TACCTGAGCACCAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2809
661 CTGCTGGAGTTCGAGCAGCGCGGATGATCACTCTCGGCATGGACGAGCTGTACAAGAG 720
2810 CTGCTGGAGTTCGAGCAGCGCGGATGATCACTCTCGGCATGGACGAGCTGTACAAGAG 2869
721 CTAGCCATGGC 732
2870 TTGGAGGTGGC 2881

Query Match 84.6%; Score 719.2; DB 12; Length 5713;
Best Local Similarity 98.9%; Pred. No. 2.8e-158;
Matches 724; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
1 ATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGGTGGTCCCATCTCTGGTCGAGCTGGAC 60
2150 ATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGGTGGTCCCATCTCTGGTCGAGCTGGAC 2209
61 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 120
2210 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 2269
121 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 180
2270 GCGGACGTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 2329
181 CTGCTGACCAACCGCTGACCTACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 240
2330 CTGCTGACCAACCGCTGACCTACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2389
241 CAGCAGACTTCTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 300
2390 CAGCAGACTTCTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2449
301 TTCAAGGACGAGCGCAACTACAAAGCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 360
2450 TTCAAGGACGAGCGCAACTACAAAGCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2509
361 GTGAACCGCATCCGATCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 420
2510 GTGAACCGCATCCGATCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2569
421 AAGCTGGAGTACAACTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 480
2570 AAGCTGGAGTACAACTTCAAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2629
481 GGCATCAAGGTGAAGTTCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 540
2630 GGCATCAAGGTGAAGTTCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2689
541 GACCACTACGAGCAAGCAACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 600
2690 GACCACTACGAGCAAGCAACCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2749
601 TACCTGAGCACCAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 660
2750 TACCTGAGCACCAGTCCGCGTGTCCGGCGAGGGCGATGCCACTACCGCTTC 2809
661 CTGCTGGAGTTCGAGCAGCGCGGATGATCACTCTCGGCATGGACGAGCTGTACAAGAG 720
2810 CTGCTGGAGTTCGAGCAGCGCGGATGATCACTCTCGGCATGGACGAGCTGTACAAGAG 2869
721 CTAGCCATGGC 732
2870 TTGGAGGTGGC 2881

PRIOR FILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent in version 3.1
SEQ ID NO 5
LENGTH: 5713
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-09-963-247A-5

RESULT 13
US-10-134-643-5
Sequence 5, Application US/10134643
Publication No. US2003011389A1
GENERAL INFORMATION:
TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and IgE Syn
APPLICANT: Ferrick, David A.
APPLICANT: Swift, Susan E.
APPLICANT: Armstrong, Randall
APPLICANT: Fox, Bryan
TITLE OF INVENTION: Secretion and Switch Rearrangement
FILE REFERENCE: A-66038-1/RMS/JUD/DLR
CURRENT APPLICATION NUMBER: US/09/963,247A
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: US 09/076,624

Qy	601	TACCTGAGCACCAGTCCGCTTCTAGCAAAAGACCCAAACGAGAACGCCGATCTCATGGTC	660
Db	3290	TACCTGAGCACCAGTCCGCTTCTAGCAAAAGACCCAAACGAGAACGCCGATCTCATGGTC	3349
Qy	661	CTGCTGAGTTCTGTACCCGCCCGGGATCACTCTCGGCTTGGCATGGACGAGCTGTACAAGAAG	720
Db	3350	CTGCTGAGTTCTGTACCCGCCCGGGATCACTCTCGGCTTGGCATGGACGAGCTGTACAAGTAA	3409
Qy	721	CTTAGCATGGTTCCCGCCGGAGGTGGAGG	751
Db	3410	AGCGGCCGCACTCTAGAGTCGACCTGCAGG	3440

RESULT 15

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US-10-429-608A-2
; Sequence 2, Application US/10429608A
; Publication No. US20040071675A1
; GENERAL INFORMATION:
; APPLICANT: MAZARAKIS, NICHOLAS
; APPLICANT: AZZOUC, MIMOUN
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 674523-2017
; CURRENT APPLICATION NUMBER: US/10/429, 608A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: PCT/GB01/04866
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: GB 0122238.9
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: GB 0102339.9
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: GB 0026943.1
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 8531
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide construct PONY8G sequence
US-10-429-608A-2

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Query Match	84.6%	Score 719;	DB 16;	Length 8531;
Best Local Similarity	97.3%;	Pred. No. 3.2e-158;		
Matches 731;	Conservative 0;	Mismatches 20;	Indels 0;	Gaps 0;
QY	1	ATGTGTGACGAGGGCGAGGAGCTGTTTCACCGGGTGTGTCCTATCTCGGTGCGAGCTGGAC	60	
Db	2690	ATGTGTGACGAGGGCGAGGAGCTGTTTCACCGGGTGTGTCCTATCTCGGTGCGAGCTGGAC	2749	
QY	61	GGGACGTAAACGGCCCAAGTTTCAGCGTGTTCGGCGAGGGCGAGTGCACCTAC	120	
Db	2750	GGGACGTAAACGGCCCAAGTTTCAGCGTGTTCGGCGAGGGCGAGTGCACCTAC	2809	
QY	121	GGCAAGCTGACCTGAAGTTCATCTGCACACCGGCAAGTGTCCGCTGCCTGCACCCACC	180	
Db	2810	GGCAAGCTGACCTGAAGTTCATCTGCACACCGGCAAGTGTCCGCTGCCTGCACCCACC	2869	
QY	181	CTCGTGACACCCCTGACCTACGGCGTGCAGTGTTCAGCGCGCTACCCCGACCAATGAAG	240	
Db	2870	CTCGTGACACCCCTGACCTACGGCGTGCAGTGTTCAGCGCGCTACCCCGACCAATGAAG	2929	
QY	241	CAGCACGACTTCTCAAGTCCGCCATCGCCGAAAGGCTACGTCCAGGAGCGCAACATCTTC	300	
Db	2930	CAGCACGACTTCTTCAAGTCCGCCATCGCCGAAAGGCTACGTCCAGGAGCGCAACATCTTC	2989	
QY	301	TTCGAAGGACGACGGCACTCAAGACCGCGCCGAGGTGAAGTTCGAGGGGCGACACCTCG	360	
Db	2990	TTCGAAGGACGACGGCACTCAAGACCGCGCCGAGGTGAAGTTCGAGGGGCGACACCTCG	3049	
QY	361	GTGACCCGATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCAC	420	